

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: JOHNSON, EUGENE M
 MILBRANDT, JEFFREY D
 KOTZBAUER, PAUL T
 LAMPE, PATRICIA A
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(ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 242

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/220,617
 (B) FILING DATE: 24 Dec. 1998
 (C) CLASSIFICATION:

E 14

(viii) ATTORNEY/AGENT INFORMATION:

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 (B) REGISTRATION NUMBER: 44,704
 (C) REFERENCE/DOCKET NUMBER: 6029-7976

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
 1 5 10 15

Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
 20 25 30

Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 35 40 45
 Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 50 55 60
 Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 65 70 75 80
 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 85 90 95
 Arg Glu Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45
 Arg Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60
 His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
 65 70 75 80
 Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
 85 90 95
 Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Gly Ala Arg Pro Xaa Gly Leu Arg Glu Leu Glu Val Ser Val Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Cys Ala Gly Ala Xaa Glu Ala Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Xaa Val Glu Ala Lys Pro Cys Cys Gly Pro Thr Ala Tyr Glu Asp
 1 5 10 15

Xaa Val Ser Phe Leu Ser Val
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe		
165	170	175
Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg		
180	185	190
Glu Cys Ala Cys Val		
195		

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser			
1	5	10	15
Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg			
20	25	30	
Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp			
35	40	45	
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala			
50	55	60	
Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile			
65	70	75	80
Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Ala Arg Pro			
85	90	95	
Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu			
100	105	110	
Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys			
115	120	125	
Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg			
130	135	140	
Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His			
145	150	155	160
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp			
165	170	175	
Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys			
180	185	190	
Ala Cys Val			
195			

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGGGTTGG	GGGCGCGGCC	TTGCGGGCTG	CGCGAGCTGG	AGGTGCGCGT	GAGCGAGCTG	60
GGCCTGGGCT	ACGCGTCCGA	CGAGACGGTG	CTGTTCCGCT	ACTGCGCAGG	CGCCTGCGAG	120
GCTGCCGCGC	GCGTCTACGA	CCTCGGGCTG	CGACGACTGC	GCCAGCGGCG	GCGCCTGCGG	180
CGGGAGCGGG	TGCGCGCGCA	GCCCTGCTGC	CGCCCGACGG	CCTACGAGGA	CGAGGTGTCC	240
TTCCCTGGACG	CGCACAGCCG	CTACCCACACG	GTGCACGAGC	TGTCGGCGCG	CGAGTGCGCC	300
TGGCGTG						306

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGGGGGCTC	GGCCTTGTGG	GCTGCGCGAG	CTCGAGGTGC	GCGTGAGCGA	GCTGGGCCTG	60
GGCTACACGT	CGGATGAGAC	CGTGCTGTT	CGCTACTGCG	CAGGCGCGTG	CGAGGCGGCC	120
ATCCGCATCT	ACGACCTGGG	CCTCGGCCGC	CTGCGCCAGC	GGAGGCGCGT	GCGCAGAGAG	180
CGGGCGCGGG	CGCACCCGTG	TTGTCGCCCC	ACGGCCTATG	AGGACGAGGT	GTCCTTCCTG	240
GACGTGCACA	GCCGCTACCA	CACGCTGCAA	GAGCTGTCGG	CGCGGGAGTG	CGCGTGCCTG	300

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCGCT	GGAAGGGCGGC	GGCCTTGGCC	TCAGTGCTCT	GCAGCTCCGT	GCTGTCCATC	60
TGGATGTGTC	GAGAGGGCCT	GCTTCTCAGC	CACCGCCTCG	GACCTGCGCT	GGTCCCCCTG	120
CACCGCCTGC	CTCGAACCCCT	GGACGCCCGG	ATTGCCGCC	TGGCCCAAGTA	CCGTGCACTC	180

CTGCAGGGGG CCCCAGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCC	240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCAGCGCG CGCGTGCAGCG GTTGGGGCG	300
CGGCCTTGCAG GGCTGCGCGA GCTGGAGGTG CGCGTGAGCG AGCTGGGCCT GGGCTACGCG	360
TCCGACGAGA CGGTGCTGTT CCGCTACTGC GCAGGCGCCT GCGAGGCTGC CGCGCGCGTC	420
TACGACCTCG GGCTGCGACG ACTGCGCCAG CGGCAGCGCC TGCAGCGGGGA GCGGGTGC	480
GCGCAGCCCT GCTGCCGCC GACGGCCTAC GAGGACGAGG TGTCCCTCCT GGACGCGCAC	540
AGCCGCTACC ACACGGTGCA CGAGCTGTCG GCGCGCGAGT GCGCCTGCGT GTGA	594

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGC ATCGCCGCC TGGCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAACCTT CTCCCTGGGC TGCCCCGCATC	240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGGCCGGG GGCTCGGCCT	300
TGTGGGCTGC GCGAGCTCGA GGTGCGCGTG AGCGAGCTGG GCCTGGGCTA CACGTCGGAT	360
GAGACCGTGC TGTTCGGCTA CTGCGCAGGC GCGTGCAGG CGGCCATCCG CATCTACGAC	420
CTGGGCCTTC GGCGCCTGCG CCAGCGGAGG CGCGTGCAGCA GAGAGCGGGC GCGGGCGCAC	480
CCGTGTTGTC GCCCGACGGC CTATGAGGAC GAGGTGTCCCT TCCTGGACGT GCACAGCCGC	540
TACCACACGC TGCAAGAGCT GTCGGCGCGG GAGTGCAGCGT GCGTGTGA	588

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCG	120

GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCATGG CCCGGCCCGT	180
GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGTGCCTCCTCCG	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTGGGTG GTCGGAGGAG	300
TCACCACTGA CGGGGTCACTC TGGAGCCCGT GGCAGGCCGA GGCCCAGG	348

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCCTC GCTGAGAACT	60
GAATTCACAT AAAGTGTGGG AACTCCC	87

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser	
1 5 10 15	
Val Leu Ser	

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser	
1 5 10 15	
Leu Leu Ser	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGGCAGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCC

57

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGGCGCT GGAAGGCAGC GGCCTTGGTG TCGCTCATCT GCAGCTCCCT GCTATCT

57

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro
 1 5 10 15

Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile
 20 25 30

Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala
 35 40 45

Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro Pro Gly Pro
 50 55 60

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC	60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCC GCCTGGCCCA GTACCGTGCA	120
CTCCTGCAGG GGGCCCCGGA TGCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGCGG	180
CCCCCAGGTC CGCGCCGTCG GGCGGGGCC CGGCAGCGGT GCGCGCGT	228

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTGGATGT GCCAGGAGGG TCTGCTCTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG	60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATGCCGC GCCTGGCCCA GTATCGCGCT	120
CTGCTCCAGG GCGCCCCCGA CGCGGTGGAG CTTCGAGAAC TTTCTCCCTG GGCTGCCCG	180
ATCCCAGGAC CGCGCCGTCG AGCGGGTCCC CGGCAGCGGT GGGCGCGG	228

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro	
1 5 10 15	
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile	
20 25 30	
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala	
35 40 45	
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro	
50 55 60	

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
 1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
 20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
 35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
 50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
 65 70 75 80

Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 85 90 95

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15

Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
 20 25 30

Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
 35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
 50 55 60

Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
 65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCAGCGCT GGAAGGCAGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCCG GGACGCCCGG ATTGCCGCC TGGCCAGTA CCGTGCACTC	180
CTGCAGGGGG CCCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCC	240
CCAGGTCCGC GCCGTGGGC GGGGCCCCGG CGGCGGGCGC CGCGT	285

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCG GGACGCCCGC ATCGCCGCC TGGCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAACTTT CTCCCTGGGC TGCCCGCATC	240
CCGGGACCGC GCCGTGGAGC GGGTCCCCGG CGTCGGCGGG CGCGG	285

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGCGCT GGAAGGCAGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120

CACCGCCTGC CTCGAACCCT GGACGCCCGG ATTGCCCGCC TGGCCCAGT

169

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG	60
CTGGGCGGCC CCCAGGTCCG CGCCGTCGGG CGGGGCCCCG GCGGCGGC GCGCGTGC	120
GGTTGGGGGC GCGGCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGC	180
TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCCGCTACTG CGCAGGCGCC TGCGAGGCTG	240
CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCGGC GCGCGGCGG	300
AGCGGGTGC CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCTTCC	360
TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GGCGCGCGAG TGCGCCTGCG	420
TGTGA	425

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGC ATCGCCCGCC TGGCCCAAGT	169

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCGCGCTCT	GCTCCAGGGC	GCCCCGACG	CGGTGGAGCT	TCGAGAACTT	TCTCCCTGGG	60
CTGCCCGCAT	CCCGGGACCG	CGCCGTCGAG	CGGGTCCCCG	GCGTCGGCGG	GCGCGGCCGG	120
GGGCTCGGCC	TTGTGGGCTG	CGCGAGCTCG	AGGTGCGCGT	GAGCGAGCTG	GGCCTGGGCT	180
ACACGTCGGA	TGAGACCGTG	CTGTTCCGCT	ACTGCGCAGG	CGCGTGCAG	GCGGCCATCC	240
GCATCTACGA	CCTGGGCCCT	CGGCGCCTGC	GCCAGCGGAG	GCCCGTGCGC	AGAGAGCGGG	300
CGCGGGCGCA	CCCGTGTGT	CGCCCGACGG	CCTATGAGGA	CGAGGTGTCC	TTCCTGGACG	360
TGCACAGCCG	CTACCACACG	CTGCAAGAGC	TGTCGGCGCG	GGAGTGCGCG	TGCGTGTGA	419

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1					5					10				15	
Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
					20				25				30		
Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
					35				40				45		
Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg	Ala	Gln	Pro	Cys	Cys	Arg
					50				55			60			
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Ala	His	Ser	Arg
					65				70			75		80	
Tyr	His	Thr	Val	His	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
					85				90						

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1					5					10				15	

Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
20							25							30	
Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
35							40							45	
Arg	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala	His	Pro	Cys	Cys	Arg
50						55					60				
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	Arg
65						70				75					80
Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
85								90							

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

IID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR
 ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site

(B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys Cys Arg Pro Xaa Ala Xaa Xaa Asp Xaa Xaa Ser Phe Leu Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys Cys Arg Pro Xaa Ala Xaa Xaa Asp Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Xaa Xaa Asp Xaa Xaa Ser Phe Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYTNGG NTA

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGNDS NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCNGMNTCRC ANSHNCCNSH RCARTANCKR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTRW ANGCNRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCNARRAANS WNAVNTCRTC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTNH TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTNH TNTTYMGNTA YTGYDSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCGCGC CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCG	120
GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT	180
GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGTC CCCGGGTCGC CTCCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGGAT GAGGCGCTGG	360
AAGGCAGCGG CCCTGGTGTG GCTCATCTGC AGCTCCCTGC TATCTGTCTG GATGTGCCAG	420
GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCCCTACG ACGCCCTCCA	480
CGCACCCCTGG ACGCCCCCAT CGCCCGCCTG GCCCAGTATC GCGCTCTGCT CCAGGGCGCC	540
CCCGACGCGG TGGAGCTTCG AGAACTTTCT CCCTGGGCTG CCCGCATCCC GGGACCGCGC	600
CGTCGAGCGG GTCCCCGGCG TCGCGGGCG CGGCCGGGGG CTCGGCCTTG TGGGCTGCGC	660
GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCGGATGA GACCGTGCTG	720
TTCCGCTACT GCGCAGGCAGC GTGCGAGGCG GCCATCCGCA TCTACGACCT GGGCCTTCGG	780

CGCCTGCGCC AGCGGAGGCG CGTGCAGA GAGCGGGCGC GGGCGCACCC GTGTTGTCGC	840
CCGACGGCCT ATGAGGACGA GGTGTCCTTC CTGGACGTGC ACAGCCGCTA CCACACGCTG	900
CAAGAGCTGT CGGCGCGGGA GTGCGCGTGC GTGTGATGCT ACCTCACGCC CCCCGACCTG	960
CGAAAGGGCC CTCCCTGCCG ACCCTCGCTG AGAACTGACT TCACATAAAG TGTGGAACT	1020
CCC	1023

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA	17
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(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly	
1 5 10 15	
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys	
20 25 30	
Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg	
35 40 45	
Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro	
50 55 60	
Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr	
65 70 75 80	
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys	
85 90	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTRTGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACGAGGTGT CCTTCCTGGA CGTACACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCACAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
CGCTACTGCG CAGGCGCGTG CGARGCGGC 29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
CGCCGACAGC TCTTGCAGCG TRTGGTA 27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
GAGCTGGGCC TGGGCTACGC GTCCGACGAG 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG 39

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTGG

29

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAATCGGG GGTGYGTCTT A

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTCTG

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCGCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1					5				10					15	

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser	Pro	Asp	Lys	Gln	Ala	Ala	Ala	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1				5					10					15	
Gln	Ala	Ala	Ala	Ala	Ser	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg
					20			25				30			
Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu
	35				40				45						
Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile
	50				55				60						
Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp
65					70			75					80		
Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys
	85					90			95						
Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser
	100					105			110						
Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala
115					120				125						
Lys	Arg	Cys	Gly	Cys	Ile										
	130														

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1				5				10					15		
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
	20				25						30				
Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
	35				40			45							

Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60

Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
 65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30

Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45

Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60

Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80

Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Cys Gly Cys Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGCCGACTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG	60
GAGAAGGTCA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGCCCG TACCCAGCAC	120
AGTCTGGTAC TGGCCCGGCT TCGAGGGCGG GGTCGAGCCC ATGGCCGACC CTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGATCAGC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CTGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGC	273

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1															15
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
	20														30
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
	35														45
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
	50														60
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
	65														80
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys	Ile		
				85											90

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1															15
Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
	20														30
Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
	35														45
Arg	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala	His	Pro	Cys	Cys	Arg
	50														60
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	Arg
	65														80
Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val	
				85											95

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1				5							10			15	
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
			20					25			30				
Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
	35					40						45			
Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr
	50				55						60				
Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro
	65				70				75			80			
Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly					
					85				90						

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala	Ser	Glu	Glu	Lys	Ile	Ile
1				5		

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA 23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAGAT TATCTT 26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA	60
CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGCAGGG TCGAGCTCAT GGCAGACCTT	120
GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACAC CATTGGCAGC	180
AGCTGCCTCA GCTCTCAGCC GCAGCTTGTG GCTGTGGTGG CTGAAGGCAG CCAGCCTGGT	240
CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT	300
TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG	336

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCAACAGC CACAAGCTGC GGCTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCCTGGGG GCCTCCCGAC TCCCCAATT

60

CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT AGGTAACAAAC

120

CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT GACCCTACCA

180

GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG ATACTGTGCT

240

GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG GCTTCGAGGG	300
CGGGGTGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA TGTGACCTTC	360
CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC TTGTGGCTGT	420
GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA GGCTGGGCTT	480
TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA GGGAAAGGAC	540
CAGG	544

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln	
1 5 10 15	
Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln	
20 25 30	
Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp	
35 40 45	
Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro Gln Leu	
50 55 60	
Ser Ala Ala Ala Cys Gly Cys Gly Gly	
65 70	

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCCT	240

CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA	300
ATCACAAGCA AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTTGCATAGG	360
AGAAGATTAA GAAGAGAAAG GGGACCTGAT T	391

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Val Xaa Xaa Leu Gly Leu Gly Tyr	
1	5

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Arg Tyr Cys Xaa Gly Xaa Cys	
1	5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Xaa Xaa Xaa Phe Leu Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro
1 5 10 15

Thr Pro Gln Phe Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu
20 25 30

Leu Tyr Leu Ala Leu Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu
35 40 45

Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu
50 55 60

Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala
65 70 75 80

Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala
85 90 95

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro
 100 105 110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln
 115 120 125

Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Leu Pro Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR
 LYSINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR
 ISOLEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "THREONINE, VALINE OR
ISOLEUCINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC
ACID OR ALANINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC
ACID OR NO AMINO ACID"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Phe Leu Asp Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
 TTYMGNAYT GYDSNGGNDS NTG 23

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
 GTNDGNGANY TGGGNYTNGG 20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
 GTNDGNGANY TGGGNYTGGG NTT 23

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
 WCNTCNARRA ANGWNNAVNTC 20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR
ALANINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC
ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR
ALANINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Xaa Xaa Leu Gly Leu Gly Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCCTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAAGA	ATTCCCTGGGG	GCCTCCCGAC	180
TCCCCAATTG	CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT	240
AGGTAACAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TGGGCCTGGG	CTATGCCTCG	GAGGAGAAGG	TCATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	420
GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCACCA	GCTATGCTGA	480

TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC	540
TTGTGGCTGT GGTGGCTGA	559

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu			
1	5	10	15
Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu			
20	25	30	
Ala Arg Leu Arg Arg Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu			
35	40	45	
Thr Leu Ser Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys			
50	55	60	
Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr			
65	70	75	80
Gln His Gly Leu Ala Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His			
85	90	95	
Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu			
100	105	110	
Asp Asp Arg His Arg Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala			
115	120	125	
Cys Gly Cys Gly Gly			
130			

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5					10				15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
	20					25						30			
Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
	35						40					45			
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
	50					55					60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr
	65					70				75				80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85					90						

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Cys	Leu	Leu	Leu	Leu	Ser	Leu
1					5					10				15	
His	Pro	Ser	Leu	Gly	Trp	Val									
					20										

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Leu	Ser	Leu
1					5					10				15	
His	Leu	Gly	Leu	Gly	Trp	Val									
					20										

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT

23

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC

35

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCCACC ACCACCACCA CCACCACAC GACGACGACG ACAAGGCCTT

60

GGCTGGTTCA TGCGA

76

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
1 5 10 15

Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
20 25 30

Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
35 40 45

Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
50 55 60

Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser
65 70 75 80

Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
85 90 95

INFORMATION FOR SEQ ID NO:142:

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

TAATACGACT CACTATAGGG GAA

23

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTGGGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTATGCTAG TTATTGCTCA GCGGT

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(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45

Arg Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60

His	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp
65					70				75					80	
Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys
				85					90					95	
Gly	Cys	Gly	Gly												
				100											

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT	50
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(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAAGCTA TGCTG	25
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(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGGGTCATC TTC	23
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(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp
1				5					10					15	
Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly															
20 25 30															
Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu															
35 40 45															
Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys															
50 55 60															
Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg															
65 70 75 80															
Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys															
85 90 95															
Cys Ser															

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys	Cys	Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp
1				5					10					15	
Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly															
20 25 30															
Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu															
35 40 45															
Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys															
50 55 60															
Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys															
65 70 75 80															
Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys															
85 90 95															
Cys Ser															

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Cys	Cys	Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp
1					5					10					15
Lys	Trp	Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly
					20				25				30		
Pro	Cys	Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu
					35				40				45		
Gly	Leu	Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys
					50			55				60			
Val	Pro	Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg
					65			70			75			80	
Thr	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys
					85				90			90		95	
Cys	Ser														

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn
1								5			10				15
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly
								20			25		30		
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe
					35			40			45				
His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe
					50			55			60				
Ala	Asn	Leu	Lys	Ser	Cys	Cys	Val	Pro	Thr	Lys	Leu	Arg	Pro	Met	Ser
					65			70			75		80		

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 85 90 95

Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
 1 5 10 15

Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
 20 25 30

Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
 35 40 45

His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
 50 55 60

Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
 65 70 75 80

Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
 85 90 95

Met Ile Val Glu Glu Cys Gly Cys Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp Gly
 1 5 10 15

Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu Gly
 20 25 30

Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His Ala
 35 40 45

Tyr	Ile	Gln	Ser	Leu	Leu	Lys	Arg	Tyr	Gln	Pro	His	Arg	Val	Pro	Ser
50						55				60					
Thr	Cys	Cys	Ala	Pro	Val	Lys	Thr	Lys	Pro	Leu	Ser	Met	Leu	Tyr	Val
65					70				75				80		
Asp	Asn	Gly	Arg	Val	Leu	Leu	Glu	His	His	Lys	Asp	Met	Ile	Val	Glu
					85			90		95					
Glu	Cys	Gly	Cys	Leu											
				100											

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn
1				5				10				15			
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly
				20				25				30			
Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala
				35				40			45				
Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala
				50				55			60				
Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp
65					70				75			80			
Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	Glu
				85				90			95				
Gly	Cys	Gly	Cys	Arg											
				100											

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn
1					5			10				15			

Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	Cys	His	Gly
20							25							30	
Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala
35							40						45		
Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	Pro	Lys	Ala
50						55						60			
Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp
65					70				75					80	
Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Val	Val	Glu
				85				90					95		
Gly	Cys	Gly	Cys	Arg											
				100											

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asp
1				5				10					15		
Asp	Trp	Ile	Val	Ala	Pro	Leu	Gly	Tyr	Asp	Ala	Tyr	Tyr	Cys	His	Gly
	20						25						30		
Lys	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Phe	Asn	Ser	Thr	Asn	His	Ala
	35						40						45		
Val	Val	Gln	Thr	Leu	Val	Asn	Asn	Met	Asn	Pro	Gly	Lys	Val	Pro	Lys
	50					55						60			
Ala	Cys	Cys	Val	Pro	Thr	Gln	Leu	Asp	Ser	Val	Ala	Met	Leu	Tyr	Leu
	65				70					75				80	
Asn	Asp	Gln	Ser	Thr	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Thr	Val
				85					90				95		
Val	Gly	Cys	Gly	Cys	Arg										
					100										

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln
1				5				10						15	
Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly
		20				25							30		
Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala
		35				40			45						
Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys
		50				55			60						
Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
		65			70			75					80		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val
				85				90					95		
Arg	Ala	Cys	Gly	Cys	His										
		100													

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu
1				5				10						15	
Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	Tyr	Tyr	Cys	Glu	Gly
		20				25			30						
Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala	Thr	Asn	His	Ala
		35				40			45						
Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val	Pro	Lys
		50				55			60						
Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		65			70			75					80		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	Arg	Asn	Met	Val	Val
				85				90					95		
Lys	Ala	Cys	Gly	Cys	His										
		100													

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Cys	Gln	Met	Gln	Thr	Leu	Tyr	Ile	Asp	Phe	Lys	Asp	Leu	Gly	Trp	His
1				5					10				15		
Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Gly	Ala	Phe	Tyr	Cys	Ser	Gly
	20					25			30						
Glu	Cys	Asn	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala
	35				40				45						
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Leu	Glu	Pro	Lys	Lys	Val	Pro	Lys
	50				55				60						
Pro	Cys	Cys	Ala	Pro	Thr	Arg	Leu	Gly	Ala	Leu	Pro	Val	Leu	Tyr	His
	65				70			75		80					
Leu	Asn	Asp	Glu	Asn	Val	Asn	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Ile	Val
	85					90			95						
Lys	Ser	Cys	Gly	Cys	His										
	100														

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Cys	Ala	Arg	Arg	Tyr	Leu	Lys	Val	Asp	Phe	Ala	Asp	Ile	Gly	Trp	Ser
1				5				10				15			
Glu	Trp	Ile	Ile	Ser	Pro	Lys	Ser	Phe	Asp	Ala	Tyr	Tyr	Cys	Ser	Gly
	20					25			30						
Ala	Cys	Gln	Phe	Pro	Met	Pro	Lys	Ser	Leu	Lys	Pro	Ser	Asn	His	Ala
	35				40				45						
Thr	Ile	Gln	Ser	Ile	Val	Arg	Ala	Val	Gly	Val	Val	Pro	Gly	Ile	Pro
	50				55			60							
Glu	Pro	Cys	Cys	Val	Pro	Glu	Lys	Met	Ser	Ser	Leu	Ser	Ile	Leu	Phe
	65				70			75		80					

Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
 85 90 95

Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
 1 5 10 15

Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
 20 25 30

Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45

Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60

Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80

Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95

Asp Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His
 1 5 10 15

Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly
 20 25 30

Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala
 35 40 45

Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro	Gly
50					55				60						
Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	Ser
65				70				75				80			
Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	Val	Val	Leu	Arg	Gln	Tyr	Glu
				85				90				95			
Asp	Met	Val	Val	Asp	Glu	Cys	Gly	Cys	Arg						
				100				105							

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp	His
1				5				10						15	
Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His	Gly
				20				25				30			
Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr	Ala
				35			40				45				
Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys	Ala
				50			55				60				
Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln	Asp
				65			70			75			80		
Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val	Asp
				85			90				95				
Glu	Cys	Gly	Cys	Gly											
				100											

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys	Arg	Arg	Thr	Ser	Leu	His	Val	Asn	Phe	Lys	Glu	Ile	Gly	Trp	Asp
1					5				10					15	

Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly
 20 25 30
 Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys
 65 70 75 80
 Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys
 85 90 95
 Val Ala Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu
 1 5 10 15
 Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly
 20 25 30
 Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly
 35 40 45
 Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln
 50 55 60
 Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg
 65 70 75 80
 Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn
 85 90 95
 Leu Leu Thr Gln His Cys Ala Cys Ile
 100 105

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser Val
 1 5 10 15
 Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Ala Cys Gly
 20 25 30
 Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val Leu
 35 40 45
 Leu Leu Lys Met Gln Ala Arg Gly Ala Thr Leu Ala Arg Pro Pro Cys
 50 55 60
 Cys Val Pro Thr Ala Tyr Thr Gly Lys Leu Leu Ile Ser Leu Ser Glu
 65 70 75 80
 Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu Cys
 85 90 95
 Gly Cys Arg

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys Glu Leu His Asp Phe Ser Leu Ser Phe Ser Gln Leu Lys Trp Asp
 1 5 10 15
 Asn Trp Ile Val Ala Pro His Ser Tyr Asn Pro Ser Tyr Cys Lys Gly
 20 25 30
 Asp Cys Pro Ser Ala Val Ser His Arg Tyr Gly Ser Pro Val His Thr
 35 40 45
 Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser
 50 55 60
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
 65 70 75 80
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala
 85 90 95
 Thr Ser Cys Thr Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
1 5 10 15

Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
20 25 30

Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
35 40 45

Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
50 55 60

Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
65 70 75 80

His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
85 90

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
1 5 10 15

Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
20 25 30

Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
35 40 45

Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
50 55 60

Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
65 70 75 80

Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
85 90 95

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu	Asp	Leu	Gln	Glu	Ala	Ser	Val	Ala	Asp	Lys	Leu	Ser	Phe	Gly	Lys
1				5				10						15	
Met	Ala	Glu	Thr	Arg	Gly	Thr	Trp	Thr	Pro	His	Gln	Gly	Asn	Asn	His
			20					25					30		
Val	Arg	Leu	Pro	Arg											
			35												

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu	Asp	Leu	Gln	Glu	Ala	Pro	Ala	Ala	Asp	Glu	Leu	Ser	Ser	Gly	Lys
1				5				10						15	
Met	Ala	Glu	Thr	Gly	Arg	Thr	Trp	Lys	Pro	His	Gln	Gly	Asn	Asn	Asn
			20					25					30		
Val	Arg	Leu	Pro	Arg											
			35												

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5				10					15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
			20					25					30		
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
					35			40					45		

Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
50							55			60					
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
65						70			75			80			
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
						85			90						

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAAGA	ATTCCTGGGG	GCCTCCCGAC	180
TCCCCAATT	CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT	240
AGGTAACAAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TGGGCCTGGG	CTATGCCCTG	GAGGAGAAGG	TCATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	420
GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGATC	AGCACCAATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	540
TTGTGGCTGT	GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAATCACAA	GCATGAGACA	600
GGCTGGGCTT	TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA	660
GGGAAAGGAC	CAGGGTTTT	TTGTTTCTTT	CTTTGCTTGC	TTGTTAGTTT	TTTTTTTTT	720
TTT						723

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAAAAAAAAAA	AAAAAACTAA	CAAGCAAGCA	AAGAAAGAAA	AAAAAAACCC	CTGGTCCTTT	60
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CCCTTCTTAT	CTTTACCTAT	GCAAATTCT	AGTAATGTCA	CCTGAGCCTT	TCAAAGCCCA	120
GCCTGTCTCA	TGCTTGTGAT	TCTGAGACAC	CAGACTGGCC	TCCTTCAGCC	ACCACAGCCA	180
CAAGCTGCAG	CTGAGAGCTG	AGGCAGCTGC	TGCCAATGGT	GCTGATCATC	AAGGAAGGTC	240
ACATCAGCAT	AGCTGGTGGG	CTGGCAGCAG	GGTCGGCCAT	GGGCTCGACC	CCGCCCTCGA	300
AGCCGGGCCA	GTACCAGACT	GTGCTGGTA	CGGGCCTCTT	GGGGACAGCT	GCCAGCACAG	360
TATCGGAAGA	TGACCTTCTC	CTCCGAGGCA	TAGCCCAGGC	CCAGCTCAGC	CACTGGTAGG	420
GTCAAGGCTCC	ACAGTCGGCA	TGAACCAGCC	AAGGCTCTTG	GAAGACGGAC	ATGGTTGTTA	480
CCTAGTGCAA	GGTAGAGTAG	GATTGTAAGG	CAAAGTGAGG	GCTTGAGAG	AAGGAATTGG	540
GGAGTCGGGA	GGCCCCCAGG	AATTCTTACC	CTGATGGGGC	GTCCAGGTCC	CTCTAGTCTC	600
TGCCATCTTC	CCAAATGAGA	GCTTATCTGC	CACAGAAGCC	TCTTGAAGAT	CAAGGACCCA	660
GCCGAGGCTC	GGGTGCAAGG	ACAGGAGCAG	CAGACACAGG	ATCCGAAGTC	TTCCTGCAGC	720
CAT						723

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAACA	ACCATGTCCG	TCTTCCAAGA	180
GCCTTGGCTG	GTTCATGCCG	ACTGTGGAGC	CTGACCTAC	CAGTGGCTGA	GCTGGGCCTG	240
GGCTATGCCT	CGGAGGAGAA	GGTCATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	300
GCCCGTACCC	AGCACAGTCT	GGTACTGGCC	CGGCTTCGAG	GGCGGGGTCG	AGCCCATGGC	360
CGACCCCTGCT	GCCAGCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	TCAGCACCAT	420
TGGCAGCAGC	TGCCTCAGCT	CTCAGCTGCA	GCTTGTGGCT	GTGGTGGCTG	A	471

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

TCAGGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC	AATGGTGCTG	60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC	GGCCATGGGC	120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG	CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCTCC GAGGCATAGC	CCAGGCCAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG	CTCTTGAAG	300
ACGGACATGG TTGTTACCT GATGGGGCGT CCAGGTCCCT CTAGTCTCTG	CCATCTTCCC	360
AAATGAGAGC TTATCTGCCA CAGAAGCCTC TTGAAGATCA AGGACCCAGC	CGAGGCTCGG	420
GTGCAAGGAC AGGAGCAGCA GACACAGGAT CCGAAGTCTT CCTGCAGCCA	T	471

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC	TGTCCTTGCA CCCGAGCCTC	60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA	AGCTCTCATT TGGGAAGATG	120
GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAACA	ACCATGTCCG TCTTCCAAGA	180

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TCTTGGAAAGA CGGACATGGT TGTACCTCTG ATGGGGCGTC	CAGGTCCCTC TAGTCTCTGC	60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAAGCCTCT	TGAAGATCAA GGACCCAGCC	120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC	CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCCTTGGCTG	GTTCATGCCG	ACTGTGGAGC	CTGACCCCTAC	CAGTGGCTGA	GCTGGGCCTG	60
GGCTATGCCT	CGGAGGAGAA	GGTCATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	120
GCCCCGTACCC	AGCACAGTCT	GGTACTGGCC	CGGCTTCGAG	GGCGGGGTG	AGCCCATGGC	180
CGACCCCTGCT	GCCAGCCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	TCAGCACCAT	240
TGGCAGCAGC	TGCCCTCAGCT	CTCAGCTGCA	GCTTGTGGCT	GTGGTGGCTG	A	291

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TCAGGCCACCA	CAGCCACAAG	CTGCAGCTGA	GAGCTGAGGC	AGCTGCTGCC	AATGGTGCTG	60
ATCATCAAGG	AAGGTACACAT	CAGCATAGCT	GGTGGGCTGG	CAGCAGGGTC	GGCCATGGGC	120
TCGACCCCCGC	CCTCGAAGCC	GGGCCAGTAC	CAGACTGTGC	TGGGTACGGG	CCTCTGGGG	180
ACAGCTGCCA	GCACAGTATC	GGAAAGATGAC	CTTCTCCTCC	GAGGCATAGC	CCAGGCCCCAG	240
CTCAGCCACT	GGTAGGGTCA	GGCTCCACAG	TCGGCATGAA	CCAGCCAAGG	C	291

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Cys	Leu	Leu	Leu	Ser	Leu
1														
														15

His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala

20	25	30
Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr		
35	40	45
Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly		
50	55	60
Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu		
65	70	75
Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser		
85	90	95
Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu		
100	105	110
Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser		
115	120	125
Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu		
130	135	140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly		
145	150	155

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

1	5	10
Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu		
15		
His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala		
20	25	30
Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr		
35	40	45
Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg		
50	55	60

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1					5					10					15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
					20				25					30	
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val
					35				40					45	
Leu	Ala	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
					50			55			60				
Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His
					65			70			75			80	
Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG	GAAGACTTCG	GATCTTGT	TTCTGCTCC	TGTCCTTGCA	CCTGGGCCTT	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTCCT	GCGGCAGATG	AGCTCTCATC	TGGGAAAATG	120
GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAAGA	ATTCTTGGGG	GCCTCCTAAC	180
TCTACAGTTC	TTCCCTCTCAA	AGCCCTCACT	TTGCCTCACA	ATCCTATTCT	ACCTTGCACT	240
AGGTAACAAAC	AATGTCCGCC	TTCCAAGAGC	CTTACCTGGT	TTGTGCCGGC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TTGGCCTGGG	CTATGCCTCA	GAGGAGAAGA	TTATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGT	CCGTACCCAG	CACAGTCTGG	TGCTGGCCCG	420
TCTTCGAGGG	CAGGGTCGAG	CTCATGGCAG	ACCTTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGACC	ACCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCCGCAGC	540
TTGTGGCTGT	GGTGGCTGA					559

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCAGGCCACCA	CAGCCACAAG	CTGCGGCTGA	GAGCTGAGGC	AGCTGCTGCC	AATGGTGGTG	60
GTCATCAAGG	AAGGTACAT	CAGCATAGCT	GGTGGGCTGG	CAGCAAGGTC	TGCCATGAGC	120
TCGACCCCTGC	CCTCGAAGAC	GGGCCAGCAC	CAGACTGTGC	TGGGTACGGA	CCTCTGGGG	180
ACAGCTGCCA	GCACAGTATC	GGAAAGATAAT	CTTCTCCTCT	GAGGCATAGC	CCAGGCCAAG	240
CTCAGCCACT	GGTAGGGTCA	GGCTCCACAG	CCGGCACAAA	CCAGGTAAGG	CTCTTGGAAAG	300
GCGGACATTG	TTGTTACCTA	GTGCAAGGTA	GAATAGGATT	GTGAGGCAA	GTGAGGGCTT	360
TGAGAGGAAG	AACTGTAGAG	TTAGGAGGCC	CCCAAGAATT	CTTACCCCTGA	TGGGGCTTCC	420
AGGTCTTCC	AGTCTCTGCC	ATTTTCCCAG	ATGAGAGCTC	ATCTGCCGCA	GGAGCCTCTT	480
GAAGATCAAG	GACCCAGCCA	AGGCCAGGT	GCAAGGACAG	GAGCAGCAGA	AAACAAGATCC	540
GAAGTCTTCC	TGCAGCCAT					559

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGGCTGCAG	GAAGACTTCG	GATCTGTTT	CTGCTGCTCC	TGTCTTGCA	CCTGGGCCTT	60
GGCTGGTCC	TTGATCTTCA	AGAGGCTCCT	GCAGCAGATG	AGCTCTCATC	TGGGAAAATG	120
GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAACA	ACAATGTCCG	CCTTCCAAGA	180
GCCTTACCTG	GTGGTGCCG	GCTGTGGAGC	CTGACCTAC	CAGTGGCTGA	GCTTGGCCTG	240
GGCTATGCCT	CAGAGGAGAA	GATTATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	300
GTCCGTACCC	AGCACAGTCT	GGTGCTGGCC	CGTCTTCGAG	GGCAGGGTCG	AGCTCATGGC	360
AGACCTTGCT	GCCAGCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	CCACCAACCAT	420
TGGCAGCAGC	TGCCTCAGCT	CTCAGCCGCA	GCTTGTGGCT	GTGGTGGCTG	A	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCAGGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAAG	300
GCGGACATTG TTGTTACCCCT GATGGGGCTT CCAGGTCTT CCAGTCTCTG CCATTTTCCC	360
AGATGAGAGC TCATCTGCCG CAGGAGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCAG	420
GTGCAAGGAC AGGAGCAGCA GAAACAAGAT CCGAAGTCTT CCTGCAGCCA T	471

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGGCTGCAG GAAGACTTCG GATCTTGTTC CTGCTGCTCC TGTCCCTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA	180

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCTTGGAAAGG CGGACATTGT TGTTACCCCTG ATGGGGCTTC CAGGTCTTC CAGTCTCTGC	60
CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC	120
AAGGCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCTTACCTG	GTTTGTGCCG	GCTGTGGAGC	CTGACCCCTAC	CAGTGGCTGA	GCTTGGCCTG	60
GGCTATGCCT	CAGAGGAGAA	GATTATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	120
GTCCGTACCC	AGCACAGTCT	GGTGCTGGCC	CGTCTTCGAG	GGCAGGGTCG	AGCTCATGGC	180
AGACCTTGCT	GCCAGCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	CCACCACCAT	240
TGGCAGCAGC	TGCCTCAGCT	CTCAGCCGCA	GCTTGTGGCT	GTGGTGGCTG	A	291

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TCAGCCACCA	CAGCCACAAG	CTGCGGCTGA	GAGCTGAGGC	AGCTGCTGCC	AATGGTGGTG	60
GTCATCAAGG	AAGGTACACAT	CAGCATAGCT	GGTGGGCTGG	CAGCAAGGTC	TGCCATGAGC	120
TCGACCCCTGC	CCTCGAAGAC	GGGCCAGCAC	CAGACTGTGC	TGGGTACGGA	CCTCTTGGGG	180
ACAGCTGCCA	GCACAGTATC	GGAAAGATAAT	CTTCTCCTCT	GAGGCATAGC	CCAGGCCAAG	240
CTCAGCCACT	GGTAGGGTCA	GGCTCCACAG	CCGGCACAAA	CCAGGTAAGG	C	291

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Ser	Leu
1														15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly
 50 55 60

Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
 65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95

Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
 100 105 110

Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
 115 120 125

Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu
 130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Ser Leu
 1 5 10 15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala	Leu	Pro	Gly	Leu	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1				5					10						15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr
	20							25							30
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val
	35						40								45
Leu	Ala	Arg	Leu	Arg	Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
	50						55								60
Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His
	65						70								80
Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
								85			90				95

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG	GTCCATGCCA	GCTGTGGAGC	CTGACCCCTGT	CCGTGGCAGA	GCTAGGCCTG	60
GGCTACGCCT	CAGAGGAGAA	GGTCATCTTC	CGCTACTGCG	CCGGCAGCTG	CCCCCGTGGT	120
GCCCCGACCC	AGCATGGCCT	GGCGCTGGCC	CGGCTGCAGG	GCCAGGGCCG	AGCCCACGGT	180
GGGCCCTGCT	GCCGGCCCAC	TCGCTACACC	GACGTGGCCT	TCCTCGATGA	CCGCCACCGC	240
TGGCAGCGGC	TGCCCCAGCT	CTCGGCGGCT	GCCTGCGGCT	GTGGTGGCTG	A	291

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCAGGCCACCA	CAGCCGCAGG	CAGCCGCCGA	GAGCTGGGGC	AGCCGCTGCC	AGCGGTGGCG	60
GTCATCGAGG	AAGGCCACGT	CGGTGTAGCG	AGTGGGCCGG	CAGCAGGGCC	CACCGTGGGC	120

TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG	60
GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGCTACTGCG CGGGCAGCTG CCCCCGTGGT	120
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	180
GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	240
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCCGTAG GGAAGTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCGT CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGAGAA GGTACATCTTC CGCTACTGCG CGGGCAGCTG CCCCCGTGGT	300
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT	360
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GCGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTGCCA CCTGTTCAGA	360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG	420
CTGCAGGGAC AGGAGCAGCA GAGAGCCCAG CAGGAACCTTC CCTACGGCCA T	471

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGCCGTAG GGAAGTTCTT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCGTG CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT	300
GCCCCCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	360
GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTGCCA CCTGTTCAAGA	360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG	420
CTGCAGGGAC AGGAGCAGCA GGGAGCCCAG CAGGAACCTTC CCTACGGCCA T	471

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGGCCGTAG GGAAGTTCTT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAACTTCCC	60
TACGGCCAT	69

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTTCTCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAACTTCCC	60
TACGGCCAT	69

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCCGATGCC	GTGGGGTTCC	CGTGGCCGAT	GGAGAGTTCT	CGTCTGAACA	GGTGGCAAAG	60
GCTGGAGGGA	CCTGGCTGGG	CACCCACCGC	CCCCTTGC	GCCTGCGCCG	A	111

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCGGCGCAGG	CGGGCAAGGG	GGCGGTGGGT	GCCCAGCCAG	GTCCCTCCAG	CCTTTGCCAC	60
CTGTTCA	GAGAACTCTC	CATCGGCCAC	GGGAACCCCA	CGGGCATCGG	G	111

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGCCGTAG	GGAAAGTTCT	GCTGGGCTCT	CTGCTGCTCC	TGTCCCTGCA	GCTGGGACAG	60
GGCTGGGGCC	CCGATGCCCG	TGGGGTTCCC	GTGGCCGATG	GAGAGTTCTC	GTCTGAACAG	120
GTGGCAAAGG	CTGGAGGGAC	CTGGCTGGGC	ACCCACCGCC	CCCTTGCCCG	CCTGCGCCGA	180

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC	60
CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC	120
CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCCAGC AGGAACTTCC CTACGGCCAT	180

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTTCTT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC	60
CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC	120
CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCCAGC AGGAACTTCC CTACGGCCAT	180

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu	
1 5 10 15	

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
 50 55 60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
 65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
 100 105 110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
 115 120 125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
 130 135 140

Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met	Ala	Val	Gly	Lys	Phe	Leu	Leu	Gly	Ser	Leu	Leu	Leu	Ser	Leu
1						5				10				15
Gln	Leu	Gly	Gln	Gly	Trp	Gly								
					20									

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro	Asp	Ala	Arg	Gly	Val	Pro	Val	Ala	Asp	Gly	Glu	Phe	Ser	Ser	Glu
1						5				10					15
Gln	Val	Ala	Lys	Ala	Gly	Gly	Thr	Trp	Leu	Gly	Thr	His	Arg	Pro	Leu
					20				25					30	
Ala	Arg	Leu	Arg	Arg											
		35													

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala	Leu	Ser	Gly	Pro	Cys	Gln	Leu	Trp	Ser	Leu	Thr	Leu	Ser	Val	Ala
1					5				10						15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
					20			25						30	
Cys	Ala	Gly	Ser	Cys	Pro	Arg	Gly	Ala	Arg	Thr	Gln	His	Gly	Leu	Ala
					35			40			45				
Leu	Ala	Arg	Leu	Gln	Gly	Gln	Gly	Arg	Ala	His	Gly	Gly	Pro	Cys	Cys
					50			55			60				
Arg	Pro	Thr	Arg	Tyr	Thr	Asp	Val	Ala	Phe	Leu	Asp	Asp	Arg	His	Arg
					65			70		75				80	
Trp	Gln	Arg	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
					85			90						95	

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGCCAGCTGT GGAGCCTGAC CCTGTCCGTG GCAGAGCTAG GCCTGGGCTA CGCCTCAGAG	60
GAGAAGGTCA TCTTCCGCTA CTGCGCCGGC AGCTGCCCCC GTGGTGCCCG CACCCAGCAT	120
GGCCTGGCGC TGGCCCGCT GCAGGGCCAG GGCGAGCCC ACGGTGGGCC CTGCTGCCGG	180
CCCACTCGCT ACACCGACGT GGCTTCCTC GATGACCGCC ACCGCTGGCA GCGGCTGCC	240
CAGCTCTCGG CGGCTGCCTG CGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu Gly	
1 5 10 15	
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys	
20 25 30	
Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu Gln	
35 40 45	
Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr	
50 55 60	
Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro	
65 70 75 80	
Gln Leu Ser Ala Ala Cys Gly Cys	
85	

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro
1 5

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS GGGCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTTCCGCTAC 60

TGCGCCGGCA GCTGCCCGG TGGTGCCCGC ACCCAGCATG GCCTGGCGCT GGCCCGGCTG 120

CAGGGCCAGG GCCGAGCCCA CGGCAGGGCCC TGCTGCCGCC CCATGGCC 168

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAGG TCATCTTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGGAGAAG GTCATCTTCC GCTA

24

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGGCCCTG GCCCTGCAGC

20

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G 31

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCTG C 31

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC 60

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG 59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:
 TCAGGCCACCA CAGCCGCAGG CAGCC

25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro
5									10					15
Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
		20							25					30
Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser
			35					40					45	
Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln
			50					55					60	
Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly		
			65					70						

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu
5									10					15
Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly
			20					25					30	
Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn
					35				40				45	

Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala
 50 55 60
 Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 65 70 75
 Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg
 80 85 90
 Cys Gly Cys

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
 85 90

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